

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Open gap  and extension gap  penalties  
gap x dropoff  expect  word size  Filter

Sequence 1 Enter accession or GI

Heavy Chain CDR1

or sequence in FASTA format from:  to:

DTYIHK

Murine 21.6

Sequence 2 Enter accession or GI

or sequence in FASTA format from:  to:

SYWMHK

residues 50-54 of  
Seq ID NO: 15

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

Credits to: Tatiana Tatusov and Tom Madden



[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Help](#)**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]**

Matrix  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 lcl|seq\_1 Length 5

Sequence 2 lcl|seq\_2 Length 5

No significant similarity was found

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Open gap  and extension gap  penalties

gap x dropoff  expect  word size  Filter

Sequence 1 Enter accession or GI

Heavy Chain CDR2

or sequence in FASTA format from:  to:

RIDPANGYTKYDPKFQG

Maine 21.6

Sequence 2 Enter accession or GI

or sequence in FASTA format from:  to:

EIDPSESNTNYNQKFKG

residues 69-85 of  
SEQ ID NO: 15

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)

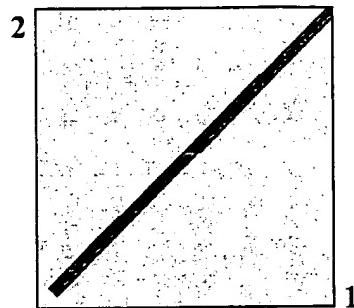
[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Help](#)

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 lcl|seq\_1 Length 17 (1 .. 17)

Sequence 2 lcl|seq\_2 Length 17 (1 .. 17)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 22.3 bits (46), Expect = 359  
 Identities = 8/16 (50%), Positives = 11/16 (68%)

Query: 2 IDPANGYTKYDPKFQG 17  
 IDP+ T Y+ KF+G  
 Sbjct: 2 IDPSESNTNYNQKFKG 17

CPU time: 0.03 user secs. 0.02 sys. secs 0.05 total secs.

Gapped:  
 Lambda: K H  
 0.270 0.0470 0.230

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 6  
 Number of Sequences: 0  
 Number of extensions: 1  
 Number of successful extensions: 1  
 Number of sequences better than 100000.0: 1  
 Number of HSP's better than 100000.0 without gapping: 1  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 1  
 length of query: 17  
 length of database: 90,077,593  
 effective HSP length: 0  
 effective length of query: 21

effective length of database: 90077593  
effective search space: 1891629453  
effective search space used: 1891629453  
T: 9  
A: 40  
X1: 17 ( 7.3 bits)  
X2: 128 (49.9 bits)  
X3: 128 (49.9 bits)  
S1: 29 (15.5 bits)  
S2: 26 (14.5 bits)

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter

Sequence 1 Enter accession or GI

Heavy Chain CDR3

or sequence in FASTA format from:  to:

EGYFGNYGVYAMDY

216 Hc

Sequence 2 Enter accession or GI

or sequence in FASTA format from:  to:

GGYDGWDYAIDY

residues 118-129 of

SEQ ID No: 15

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)



[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Help](#)**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]**

Matrix  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 lcl|seq\_1 Length 14

Sequence 2 lcl|seq\_2 Length 12

No significant similarity was found